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RAW SEQUENCE LISTING

DATE: 11/26/2001

PATENT APPLICATION: US/09/877,665

TIME: 11:30:31

Input Set : N:\Crif3\RULE60\09877665.txt

Output Set: C:\CRF31113\REFHOLD\I877665.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

7 (ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related

8 Ligands and Uses Therefor

10 (iii) NUMBER OF SEQUENCES: 23

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Genentech, Inc.

14 (B) STREET: 1 DNA Way

15 (C) CITY: South San Francisco

16 (D) STATE: California

17 (E) COUNTRY: USA

18 (F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: WinPatin (Genentech)

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/877,665

C--> 28 (B) FILING DATE: 08-Jun-2001

29 (C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: 09/109,206

32 (B) FILING DATE: 1998-06-30

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Conley, Deirdre L.

35 (B) REGISTRATION NUMBER: 36,487

36 (C) REFERENCE/DOCKET NUMBER: P1084R1-1

38 (ix) TELECOMMUNICATION INFORMATION:

39 (A) TELEPHONE: 650/225-2066

40 (B) TELEFAX: 650/952-9881

41 (2) INFORMATION FOR SEQ ID NO: 1:

43 (i) SEQUENCE CHARACTERISTICS:

44 (A) LENGTH: 2538 base pairs

45 (B) TYPE: Nucleic Acid

46 (C) STRANDEDNESS: Single

47 (D) TOPOLOGY: Linear

49 (ix) FEATURE:

50 (A) NAME/KEY: mouse NRG3 nucleic acid

51 (B) LOCATION: 1-2538

52 (C) IDENTIFICATION METHOD:

53 (D) OTHER INFORMATION:

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

58 CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCCTCT ACCGAGCGGCC 50

60 TCGCCGCCCC CTCCCCGGCC CGCGTCCCCCT CCCCCGTCTCT CTCCTCCCCG 100

62 CCCGCCGCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150

ENTERED

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```
64 GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200
66 GCCCCGCCCC GCGCCCGCGC CCGGCCCCGCG CGGCCCCATG CCTCTGGCGC 250
68 GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300
70 GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350
72 CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GGCGGCGGCG GGCGGGGGCC 400
74 CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCCGGA GTTACGCTGT 450
76 AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500
78 TCTGTTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550
80 GGATCGTGTT AGGCTCCGTC AAGGAGTACG TGCCCACGGA CCTGGTGAC 600
82 TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650
84 CCCCAGGGCT ATGGAAAACA CCACAACAAC CACTTCTACC ACGTCCCCCG 700
86 CCACCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750
88 AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800
90 CCGGGTTCCC ATCCGGGCTA GCCCGCGCTC TACCACAGCA CGGAACACTG 850
92 CTGCCCCCTC GACGGTCCTG TCCACCACGG CCCCTTCTT CAGTAGCAGC 900
94 ACGCCCGGCT CCCGACCCCG GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950
96 GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000
98 CCACTCCCTC CTGGACCCTG TCACCTTTC AGGATGCTGC TGCCGCCTCT 1050
100 TCCTCCTCAC CCTCTTCCAC CTCTCCACT ACCACCACCC CAGAAACTAG 1100
102 CACCAGCCCC AAATTTTCATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150
104 ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200
106 GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAGC ACTGTCGGTG 1250
108 CAAGGAAGGC TACCAAGGAG TCCGTGTGA TCAATTTCTG CCGAAAACAG 1300
110 ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
112 AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTCTAT GTATCATCTT 1400
114 TGGAAATGTC ATCGTGGGCA TGTTCGTGC AGCATTTCTAC TTCAAAAGCA 1450
116 AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAGAGTC ACAGAAATGGG 1500
118 AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
120 GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600
122 CTGCGCTGGA GAAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTT 1650
124 CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
126 CCCAGGACAA AGGAGTGGGA TGTTCATAG GAATACTTTC AGAAGGGCAC 1750
128 CACCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
130 CAACTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
132 GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
134 TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
136 CAAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
138 TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050
140 CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
142 CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACCTC 2150
144 CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
146 TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
148 ATCCGGATTC TGAATGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
150 CATGGAAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350
152 GTCCACGGC CAAATCAGAA CGAGAGGCAC AATTGTCTT AAGAAATGAA 2400
154 ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450
156 GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500
158 TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538
160 (2) INFORMATION FOR SEQ ID NO: 2:
```

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```

162      (i) SEQUENCE CHARACTERISTICS:
163          (A) LENGTH: 713 amino acids
164          (B) TYPE: Amino Acid
165          (D) TOPOLOGY: Linear
167      (ix) FEATURE:
168          (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
169          (B) LOCATION: 1-713
170          (C) IDENTIFICATION METHOD:
171          (D) OTHER INFORMATION:
173      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
175 Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser
176   1           5           10           15
178 Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala
179           20           25           30
181 Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala
182           35           40           45
184 Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp
185           50           55           60
187 Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly
188           65           70           75
190 Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val
191           80           85           90
193 Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser
194           95          100          105
196 Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser
197          110          115          120
199 Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr
200          125          130          135
202 Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr
203          140          145          150
205 Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro
206          155          160          165
208 Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg
209          170          175          180
211 Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser
212          185          190          195
214 Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro
215          200          205          210
217 Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro
218          215          220          225
220 Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro
221          230          235          240
223 Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ala Ala Ser Ser
224          245          250          255
226 Ser Ser Pro Ser Ser Thr Ser Ser Thr Thr Thr Thr Pro Glu Thr
227          260          265          270
229 Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg
230          275          280          285
232 Ser Glu His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys

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233		290		295		300
235	Leu Asn Asp Gly	Glu Cys Phe Val Ile	Glu Thr Leu Thr Gly	Ser		
236		305		310		315
238	His Lys His Cys	Arg Cys Lys Glu Gly	Tyr Gln Gly Val Arg	Cys		
239		320		325		330
241	Asp Gln Phe Leu	Pro Lys Thr Asp Ser	Ile Leu Ser Asp Pro	Thr		
242		335		340		345
244	Asp His Leu Gly	Ile Glu Phe Met Glu	Ser Glu Asp Val Tyr	Gln		
245		350		355		360
247	Arg Gln Val Leu	Ser Ile Ser Cys Ile	Ile Phe Gly Ile Val	Ile		
248		365		370		375
250	Val Gly Met Phe	Cys Ala Ala Phe Tyr	Phe Lys Ser Lys Lys	Gln		
251		380		385		390
253	Ala Lys Gln Ile	Gln Glu His Leu Lys	Glu Ser Gln Asn Gly	Lys		
254		395		400		405
256	Asn Tyr Ser Leu	Lys Ala Ser Ser Thr	Lys Ser Glu Ser Leu	Met		
257		410		415		420
259	Lys Ser His Val	His Leu Gln Asn Tyr	Ser Lys Ala Asp Arg	His		
260		425		430		435
262	Pro Val Thr Ala	Leu Glu Lys Ile Met	Glu Ser Ser Phe Ser	Ala		
263		440		445		450
265	Pro Gln Ser Phe	Pro Glu Val Thr Ser	Pro Asp Arg Gly Ser	Gln		
266		455		460		465
268	Pro Ile Lys His	His Ser Pro Gly Gln	Arg Ser Gly Met Leu	His		
269		470		475		480
271	Arg Asn Thr Phe	Arg Arg Ala Pro Pro	Ser Pro Arg Ser Arg	Leu		
272		485		490		495
274	Gly Gly Ile Val	Gly Pro Ala Tyr Gln	Gln Leu Glu Glu Ser	Arg		
275		500		505		510
277	Ile Pro Asp Gln	Asp Thr Ile Pro Cys	Gln Gly Ile Glu Val	Arg		
278		515		520		525
280	Lys Thr Ile Ser	His Leu Pro Ile Gln	Leu Trp Cys Val Glu	Arg		
281		530		535		540
283	Pro Leu Asp Leu	Lys Tyr Val Ser Asn	Gly Leu Arg Thr Gln	Gln		
284		545		550		555
286	Asn Ala Ser Ile	Asn Met Gln Leu Pro	Ser Arg Glu Thr Asn	Pro		
287		560		565		570
289	Tyr Phe Asn Ser	Leu Asp Gln Lys Asp	Leu Val Gly Tyr Leu	Ser		
290		575		580		585
292	Pro Arg Ala Asn	Ser Val Pro Ile Ile	Pro Ser Met Gly Leu	Glu		
293		590		595		600
295	Glu Thr Cys Met	Gln Met Pro Gly Ile	Ser Asp Val Lys Ser	Ile		
296		605		610		615
298	Lys Trp Cys Lys	Asn Ser Tyr Ser Ala	Asp Ile Val Asn Ala	Ser		
299		620		625		630
301	Met Pro Val Ser	Asp Cys Leu Leu Glu	Glu Gln Gln Glu Val	Lys		
302		635		640		645
304	Ile Leu Leu Glu	Thr Val Gln Glu Gln	Ile Arg Ile Leu Thr	Asp		
305		650		655		660

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```

307 Ala Arg Arg Ser Glu Asp Phe Glu Leu Ala Ser Met Glu Thr Glu
308                               665                               670                               675
310 Asp Ser Ala Ser Glu Asn Thr Ala Phe Leu Pro Leu Ser Pro Thr
311                               680                               685                               690
313 Ala Lys Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile
314                               695                               700                               705
316 Gln Arg Asp Ser Val Leu Thr Lys
317                               710                               713
319 (2) INFORMATION FOR SEQ ID NO: 3:
321   (i) SEQUENCE CHARACTERISTICS:
322       (A) LENGTH: 362 amino acids
323       (B) TYPE: Amino Acid
324       (D) TOPOLOGY: Linear
326   (ix) FEATURE:
327       (A) NAME/KEY: mNRG3 extracellular domainAmino acid seq
328       (B) LOCATION: 1-362
329       (C) IDENTIFICATION METHOD:
330       (D) OTHER INFORMATION:
332   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
334 Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser
335   1           5           10           15
337 Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala
338           20           25           30
340 Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala
341           35           40           45
343 Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp
344           50           55           60
346 Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly
347           65           70           75
349 Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val
350           80           85           90
352 Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser
353           95          100          105
355 Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser
356          110          115          120
358 Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr
359          125          130          135
361 Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr
362          140          145          150
364 Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro
365          155          160          165
367 Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg
368          170          175          180
370 Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser
371          185          190          195
373 Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro
374          200          205          210
376 Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro
377          215          220          225

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Pos. 130

Seq#:21; Pos. 343,363,386,398,410,423,430,448,454

VERIFICATION SUMMARY

DATE: 11/26/2001

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Input Set : N:\Crf3\RULE60\09877665.txt

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]